

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:43:57 ; Search time 254.305 Seconds  
(without alignments)  
557.351 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 310  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2588894

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
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6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	310	100.0	401	7	ADF28528	Adf28528 NgRHy mut
2	310	100.0	420	5	AAO21477	Aao21477 Human NgR
3	310	100.0	420	6	ABR55621	Abr55621 Amino aci
4	310	100.0	420	7	ADF28510	Adf28510 NgRHy pre
5	310	100.0	420	8	ADS10516	Ads10516 Human the
6	300	96.8	419	8	ADM72131	Adm72131 Human NTR
7	291	93.9	401	6	AAE33486	Aae33486 Human REM

8	291	93.9	401	7	ADE07875	Ade07875 Novel pro
9	280	90.3	390	5	AAO21482	Aao21482 Mature hu
10	280	90.3	390	7	ADF28529	Adf28529 NgRHy mat
11	150	48.4	512	7	ADC13559	Adc13559 Human NOV
12	141	45.5	286	8	ADT77787	Adt77787 Rat Nogo
13	141	45.5	420	6	ABR55628	Abr55628 Amino aci
14	141	45.5	420	8	ADT77788	Adt77788 Rat Nogo
15	141	45.5	452	8	ADT77808	Adt77808 Chimeric
16	141	45.5	452	8	ADT77802	Adt77802 Chimeric
17	141	45.5	474	8	ADT77796	Adt77796 Chimeric
18	133	42.9	241	4	ABG15171	Abg15171 Novel hum
19	126	40.6	807	4	ABG15173	Abg15173 Novel hum
20	56	18.1	56	4	AAM23826	Aam23826 Human EST
21	56	18.1	56	7	ADE08958	Ade08958 Novel pro
22	56	18.1	56	8	ADS11791	Ads11791 Human the
23	50	16.1	51	7	ADF28526	Adf28526 Leucine-r
24	44	14.2	114	2	AAY10843	Aay10843 Amino aci
25	44	14.2	114	7	ADB47833	Adb47833 Novel hum
26	44	14.2	114	8	ADJ55388	Adj55388 Novel hum
27	44	14.2	114	9	AED67371	Aed67371 Human imm
28	33	10.6	492	4	ABG15172	Abg15172 Novel hum
29	30	9.7	30	7	ADF28512	Adf28512 NgRHy sig
30	25	8.1	25	7	ADF28520	Adf28520 Leucine-r
31	24	7.7	24	7	ADF28524	Adf28524 Leucine-r
32	24	7.7	24	7	ADF28525	Adf28525 Leucine-r
33	24	7.7	24	7	ADF28523	Adf28523 Leucine-r
34	24	7.7	24	7	ADF28522	Adf28522 Leucine-r
35	24	7.7	24	7	ADF28519	Adf28519 Leucine-r
36	24	7.7	24	7	ADF28521	Adf28521 Leucine-r
37	22	7.1	22	7	ADF28518	Adf28518 Leucine-r
38	15	4.8	15	7	ADF28513	Adf28513 PR00019A
39	15	4.8	15	7	ADF28515	Adf28515 PR00019A
40	15	4.8	15	7	ADF28516	Adf28516 PR00019B
41	15	4.8	15	7	ADF28514	Adf28514 PR00019B
42	15	4.8	15	7	ADF28517	Adf28517 PR00019B
43	11	3.5	11	8	ADT77816	Adt77816 Rat Nogo
44	11	3.5	49	6	ABR62021	Abr62021 Mouse Nog
45	11	3.5	49	6	ABR62022	Abr62022 Rat Nogo

# ALIGNMENTS

## RESULT 1

ADF28528

ID ADF28528 standard; protein; 401 AA.

XX

AC ADF28528;

XX

DT 12-FEB-2004 (first entry)

XX

DE NgRHy mutant protein lacking transmembrane domain - SED ID 438.

XX

KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;

KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;

KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;

KW paralysis; seizure; memory disorder; adiponectin; Clq domain;

OM protein - protein search, using sw model

Run on: June 20, 2006, 11:59:16 ; Search time 37.3051 Seconds  
 (without alignments)  
 727.367 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
 Perfect score: 310  
 Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649019

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	44	14.2	115	2	US-09-774-639-154	Sequence 154, App
2	11	3.5	380	2	US-09-461-325-161	Sequence 161, App
3	11	3.5	380	2	US-10-012-542-161	Sequence 161, App
4	11	3.5	380	2	US-10-115-123-161	Sequence 161, App
5	11	3.5	473	2	US-09-949-016-8448	Sequence 8448, App
6	11	3.5	473	2	US-09-999-833A-400	Sequence 400, App
7	11	3.5	473	2	US-10-020-445A-400	Sequence 400, App
8	11	3.5	473	2	US-09-978-189-400	Sequence 400, App
9	11	3.5	473	2	US-10-017-085A-400	Sequence 400, App
10	11	3.5	473	3	US-10-145-129A-400	Sequence 400, App

11	11	3.5	473	3	US-10-013-929A-400	Sequence 400, App
12	11	3.5	473	3	US-10-013-917A-400	Sequence 400, App
13	8	2.6	125	2	US-09-269-410-11	Sequence 11, Appl
14	8	2.6	226	2	US-09-489-039A-10549	Sequence 10549, A
15	8	2.6	256	2	US-09-252-991A-17168	Sequence 17168, A
16	8	2.6	305	2	US-09-489-039A-7371	Sequence 7371, Ap
17	8	2.6	320	2	US-09-248-796A-16573	Sequence 16573, A
18	8	2.6	446	2	US-09-252-991A-23809	Sequence 23809, A
19	8	2.6	455	2	US-09-793-998-8	Sequence 8, Appli
20	8	2.6	799	3	US-09-396-985B-4	Sequence 4, Appli
21	8	2.6	839	3	US-09-396-985B-2	Sequence 2, Appli
22	8	2.6	839	3	US-09-396-985B-98	Sequence 98, Appl
23	8	2.6	844	2	US-09-949-016-9438	Sequence 9438, Ap
24	8	2.6	990	2	US-10-101-464A-814	Sequence 814, App
25	8	2.6	1016	2	US-09-252-991A-25429	Sequence 25429, A
26	7	2.3	30	2	US-09-402-532-9	Sequence 9, Appli
27	7	2.3	33	2	US-09-402-532-10	Sequence 10, Appl
28	7	2.3	70	2	US-09-107-532A-4266	Sequence 4266, Ap
29	7	2.3	79	2	US-09-902-540-14223	Sequence 14223, A
30	7	2.3	88	2	US-09-489-847-173	Sequence 173, App
31	7	2.3	99	2	US-09-328-352-7239	Sequence 7239, Ap
32	7	2.3	150	2	US-09-270-767-34661	Sequence 34661, A
33	7	2.3	150	2	US-09-270-767-49878	Sequence 49878, A
34	7	2.3	185	2	US-10-101-464A-519	Sequence 519, App
35	7	2.3	195	2	US-09-583-110-4761	Sequence 4761, Ap
36	7	2.3	197	2	US-09-270-767-36125	Sequence 36125, A
37	7	2.3	197	2	US-09-270-767-51342	Sequence 51342, A
38	7	2.3	198	2	US-09-107-433-4622	Sequence 4622, Ap
39	7	2.3	209	2	US-09-973-278-267	Sequence 267, App
40	7	2.3	210	2	US-09-227-357-195	Sequence 195, App
41	7	2.3	213	2	US-09-328-352-6050	Sequence 6050, Ap
42	7	2.3	222	2	US-09-248-796A-15754	Sequence 15754, A
43	7	2.3	260	2	US-09-902-540-10767	Sequence 10767, A
44	7	2.3	268	2	US-10-104-047-3172	Sequence 3172, Ap
45	7	2.3	269	2	US-09-252-991A-20218	Sequence 20218, A

#### ALIGNMENTS

##### RESULT 1

US-09-774-639-154

; Sequence 154, Application US/09774639

; Patent No. 6806351

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 90 Human Secreted Proteins

; FILE REFERENCE: PZ013P1

; CURRENT APPLICATION NUMBER: US/09/774,639

; CURRENT FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 371

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 154

; LENGTH: 115

; TYPE: PRT

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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:15:51 ; Search time 129.254 Seconds  
(without alignments)  
1110.962 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 310  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096261

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	310	100.0	401	5	US-10-496-905-438	Sequence 438, App
2	310	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
3	310	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
4	310	100.0	420	5	US-10-496-905-420	Sequence 420, App
5	310	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
6	291	93.9	401	5	US-10-477-714-17	Sequence 17, Appl
7	280	90.3	390	3	US-09-972-546-8	Sequence 8, Appli
8	280	90.3	390	5	US-10-735-256-8	Sequence 8, Appli
9	280	90.3	390	5	US-10-496-905-439	Sequence 439, App
10	150	48.4	512	4	US-10-188-248-38	Sequence 38, Appl
11	141	45.5	420	5	US-10-491-810A-25	Sequence 25, Appl

12	133	42.9	241	5	US-10-450-763-45530	Sequence 45530, A
13	126	40.6	807	5	US-10-450-763-45532	Sequence 45532, A
14	50	16.1	51	5	US-10-496-905-436	Sequence 436, App
15	44	14.2	114	3	US-09-969-730-116	Sequence 116, App
16	44	14.2	114	4	US-10-621-363-116	Sequence 116, App
17	44	14.2	114	5	US-10-986-501-116	Sequence 116, App
18	44	14.2	115	3	US-09-774-639-154	Sequence 154, App
19	33	10.6	492	5	US-10-450-763-45531	Sequence 45531, A
20	30	9.7	30	5	US-10-496-905-422	Sequence 422, App
21	25	8.1	25	5	US-10-496-905-430	Sequence 430, App
22	24	7.7	24	5	US-10-496-905-429	Sequence 429, App
23	24	7.7	24	5	US-10-496-905-431	Sequence 431, App
24	24	7.7	24	5	US-10-496-905-432	Sequence 432, App
25	24	7.7	24	5	US-10-496-905-433	Sequence 433, App
26	24	7.7	24	5	US-10-496-905-434	Sequence 434, App
27	24	7.7	24	5	US-10-496-905-435	Sequence 435, App
28	22	7.1	22	5	US-10-496-905-428	Sequence 428, App
29	15	4.8	15	5	US-10-496-905-423	Sequence 423, App
30	15	4.8	15	5	US-10-496-905-424	Sequence 424, App
31	15	4.8	15	5	US-10-496-905-425	Sequence 425, App
32	15	4.8	15	5	US-10-496-905-426	Sequence 426, App
33	15	4.8	15	5	US-10-496-905-427	Sequence 427, App
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35	11	3.5	49	4	US-10-006-002-2	Sequence 2, Appli
36	11	3.5	49	4	US-10-006-002-3	Sequence 3, Appli
37	11	3.5	49	4	US-10-127-058-1	Sequence 1, Appli
38	11	3.5	49	4	US-10-127-058-2	Sequence 2, Appli
39	11	3.5	49	4	US-10-127-058-3	Sequence 3, Appli
40	11	3.5	283	3	US-09-972-599A-55	Sequence 55, Appl
41	11	3.5	310	6	US-11-055-163-7	Sequence 7, Appli
42	11	3.5	310	6	US-11-055-163-9	Sequence 9, Appli
43	11	3.5	344	6	US-11-055-163-6	Sequence 6, Appli
44	11	3.5	344	6	US-11-055-163-8	Sequence 8, Appli
45	11	3.5	380	4	US-10-012-542-161	Sequence 161, App

#### ALIGNMENTS

#### RESULT 1

US-10-496-905-438

; Sequence 438, Application US/10496905

; Publication No. US20050192215A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Malabika

; APPLICANT: Tang, Y. Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Zhao, Qing

; APPLICANT: Xu, Chongjun

; APPLICANT: Mulero, Julio J

; APPLICANT: Boyle, Bryan J.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

; FILE REFERENCE: HYS-B1CIP/US

; CURRENT APPLICATION NUMBER: US/10/496,905

; CURRENT FILING DATE: 2004-05-26

OM protein - protein search, using sw model

Run on: June 20, 2006, 12:16:16 ; Search time 13.661 Seconds  
 (without alignments)  
 511.862 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
 Perfect score: 310  
 Sequence: 1 MLPGLRRLQLAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 96747 seqs, 22556637 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96734

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
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 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
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 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9	2.9	426	6	US-10-449-902-37107	Sequence 37107, A
2	7	2.3	30	6	US-10-449-902-34272	Sequence 34272, A
3	7	2.3	47	6	US-10-449-902-33749	Sequence 33749, A
4	7	2.3	50	6	US-10-449-902-33780	Sequence 33780, A
5	7	2.3	86	6	US-10-953-349-30624	Sequence 30624, A
6	7	2.3	100	6	US-10-953-349-39452	Sequence 39452, A
7	7	2.3	203	6	US-10-953-349-36158	Sequence 36158, A
8	7	2.3	237	7	US-11-293-697-4647	Sequence 4647, Ap
9	7	2.3	238	6	US-10-953-349-38587	Sequence 38587, A

10	7	2.3	247	6	US-10-953-349-36157	Sequence 36157, A
11	7	2.3	278	6	US-10-953-349-4307	Sequence 4307, Ap
12	7	2.3	306	6	US-10-953-349-4306	Sequence 4306, Ap
13	7	2.3	319	6	US-10-449-902-45409	Sequence 45409, A
14	7	2.3	330	6	US-10-953-349-5740	Sequence 5740, Ap
15	7	2.3	332	6	US-10-953-349-5739	Sequence 5739, Ap
16	7	2.3	358	6	US-10-449-902-34744	Sequence 34744, A
17	7	2.3	359	6	US-10-953-349-31281	Sequence 31281, A
18	7	2.3	389	6	US-10-449-902-44348	Sequence 44348, A
19	7	2.3	434	6	US-10-471-571A-5060	Sequence 5060, Ap
20	7	2.3	470	6	US-10-953-349-31280	Sequence 31280, A
21	7	2.3	492	6	US-10-953-349-31279	Sequence 31279, A
22	7	2.3	503	6	US-10-953-349-26067	Sequence 26067, A
23	7	2.3	587	7	US-11-293-697-4811	Sequence 4811, Ap
24	7	2.3	596	6	US-10-449-902-45371	Sequence 45371, A
25	7	2.3	621	7	US-11-106-014-56	Sequence 56, Appl
26	7	2.3	692	6	US-10-196-749-560	Sequence 560, App
27	7	2.3	719	7	US-11-293-697-3841	Sequence 3841, Ap
28	7	2.3	1043	7	US-11-293-697-3097	Sequence 3097, Ap
29	7	2.3	1084	6	US-10-449-902-52915	Sequence 52915, A
30	7	2.3	1144	6	US-10-449-902-42914	Sequence 42914, A
31	6	1.9	11	7	US-11-122-986-354	Sequence 354, App
32	6	1.9	30	7	US-11-122-986-829	Sequence 829, App
33	6	1.9	36	6	US-10-449-902-39872	Sequence 39872, A
34	6	1.9	43	6	US-10-449-902-34194	Sequence 34194, A
35	6	1.9	44	7	US-11-299-304-100	Sequence 100, App
36	6	1.9	48	7	US-11-264-029-28	Sequence 28, Appl
37	6	1.9	64	6	US-10-449-902-55173	Sequence 55173, A
38	6	1.9	80	6	US-10-449-902-36288	Sequence 36288, A
39	6	1.9	83	6	US-10-449-902-35748	Sequence 35748, A
40	6	1.9	85	6	US-10-449-902-48165	Sequence 48165, A
41	6	1.9	86	6	US-10-501-834-23	Sequence 23, Appl
42	6	1.9	87	6	US-10-953-349-30981	Sequence 30981, A
43	6	1.9	92	6	US-10-953-349-25928	Sequence 25928, A
44	6	1.9	92	6	US-10-953-349-38189	Sequence 38189, A
45	6	1.9	92	6	US-10-953-349-38682	Sequence 38682, A

#### ALIGNMENTS

##### RESULT 1

US-10-449-902-37107

; Sequence 37107, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870



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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:52:46 ; Search time 26.7966 Seconds  
(without alignments)  
1113.096 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 310  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	8	2.6	181	2	AC0550	shikimate kinase I	
2	8	2.6	244	2	JC8019	CD58 protein - pig	
3	8	2.6	262	1	B64154	probable radical-f	
4	8	2.6	337	2	D70120	probable Na <sup>+</sup> /Ca <sup>2+</sup> -	
5	8	2.6	481	2	T33733	hypothetical prote	
6	8	2.6	925	2	H96638	protein T1F9.20 [i	
7	8	2.6	967	2	G96637	hypothetical prote	
8	8	2.6	1148	2	D85360	hypothetical prote	
9	8	2.6	1986	2	S28353	probable polyketid	
10	7	2.3	60	2	AD2255	hypothetical prote	
11	7	2.3	62	2	T28346	ORF MSV185 hypothe	
12	7	2.3	70	2	S53706	cytochrome-c oxida	
13	7	2.3	78	2	AD2707	hypothetical prote	

14	7	2.3	83	2	D70639	hypothetical prote
15	7	2.3	132	1	B64104	virulence-associat
16	7	2.3	147	1	HBLUA	hemoglobin beta ch
17	7	2.3	154	2	T07767	disease resistance
18	7	2.3	154	2	T07769	disease resistance
19	7	2.3	157	2	G84292	hypothetical prote
20	7	2.3	159	2	A72679	hypothetical prote
21	7	2.3	164	2	T51261	hypothetical prote
22	7	2.3	168	2	B69776	hypothetical prote
23	7	2.3	191	2	AD0812	probable lipoprote
24	7	2.3	212	2	B75156	resolvase related
25	7	2.3	216	2	T37221	hypothetical prote
26	7	2.3	219	2	F83160	two-component resp
27	7	2.3	223	2	E83596	DNA mismatch repai
28	7	2.3	225	2	T11279	H <sup>+</sup> -transporting tw
29	7	2.3	237	2	T26765	hypothetical prote
30	7	2.3	238	2	AH0338	histidine transpor
31	7	2.3	240	1	ZIZM2	19K zein precursor
32	7	2.3	240	1	ZIZM91	19K zein precursor
33	7	2.3	240	1	ZIZM92	19K zein precursor
34	7	2.3	240	2	A22831	19K zein precursor
35	7	2.3	241	2	AG0857	hypothetical prote
36	7	2.3	250	2	S75302	hypothetical prote
37	7	2.3	252	2	T01787	thyrotropin recept
38	7	2.3	253	1	JC1319	thyrotropin recept
39	7	2.3	253	2	T00290	psiA protein - Esc
40	7	2.3	260	2	T18554	integral membrane
41	7	2.3	264	2	G83245	probable ATP-bindi
42	7	2.3	277	2	D82392	conserved hypothet
43	7	2.3	283	2	E83053	dihydropteroate sy
44	7	2.3	285	2	A40657	hypothetical prote
45	7	2.3	290	2	G95397	probable LysR-fami

#### ALIGNMENTS

##### RESULT 1

AC0550

shikimate kinase II [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C;Accession: AC0550

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

OM protein - protein search, using sw model

Run on: June 20, 2006, 11:44:20 ; Search time 201.763 Seconds  
 (without alignments)  
 1421.248 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
 Perfect score: 310  
 Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_7.2:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	310	100.0	420	1 R4RL2_HUMAN	Q86un3 homo sapien
2	141	45.5	420	1 R4RL2_RAT	Q80wd1 rattus norv
3	125	40.3	420	1 R4RL2_MOUSE	Q7m6z0 mus musculu
4	12	3.9	310	2 Q4RRQ4_TETNG	Q4rrq4 tetraodon n
5	12	3.9	324	2 Q4S3K9_TETNG	Q4s3k9 tetraodon n
6	12	3.9	411	2 Q4S6L6_TETNG	Q4s6l6 tetraodon n
7	12	3.9	412	2 Q4RRU8_TETNG	Q4rru8 tetraodon n
8	12	3.9	457	2 Q6WZD1_BRARE	Q6wzd1 brachydanio
9	12	3.9	478	2 Q6WZD2_BRARE	Q6wzd2 brachydanio
10	11	3.5	473	1 RTN4R_HUMAN	Q9bzt6 homo sapien
11	11	3.5	473	1 RTN4R_MACFA	Q9n0e3 macaca fasc
12	11	3.5	473	1 RTN4R_MOUSE	Q99pi8 mus musculu
13	11	3.5	473	1 RTN4R_RAT	Q99m75 rattus norv
14	10	3.2	265	2 Q3PEZ7_PARDE	Q3pez7 paracoccus
15	10	3.2	441	1 R4RL1_HUMAN	Q86un2 homo sapien

16	10	3.2	445	1	R4RL1_MOUSE	Q8k0s5	mus musculu
17	10	3.2	445	1	R4RL1_RAT	Q80wd0	rattus norv
18	9	2.9	321	2	Q3MSG3_KLEOX	Q3msg3	klebsiella
19	9	2.9	321	2	Q3MSI6_KLEPN	Q3msi6	klebsiella
20	9	2.9	400	2	Q45WB1_TOXGO	Q45wb1	toxoplasma
21	9	2.9	426	2	Q655P5_ORYSA	Q655p5	oryza sativ
22	9	2.9	458	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
23	9	2.9	479	2	Q6DH76_BRARE	Q6dh76	brachydanio
24	9	2.9	479	2	Q6X3Y5_BRARE	Q6x3y5	brachydanio
25	9	2.9	686	2	Q5FLT7_LACAC	Q5flt7	lactobacill
26	9	2.9	1207	2	Q2JZJ1_RHIET	Q2jzj1	rhizobium e
27	8	2.6	76	2	Q5FE50_EHRRW	Q5fe50	ehrlichia r
28	8	2.6	87	2	Q6J1Q3_9CAUD	Q6j1q3	burkholderi
29	8	2.6	88	2	Q4KIV0_PSEF5	Q4kiv0	pseudomonas
30	8	2.6	93	2	Q3ITV5_NATPD	Q3itv5	natronomona
31	8	2.6	118	2	Q7U642_SYNPX	Q7u642	synechococc
32	8	2.6	119	2	Q6FA35_ACIAD	Q6fa35	acinetobact
33	8	2.6	122	1	INSL3_MOUSE	O09107	mus musculu
34	8	2.6	122	2	Q5RL10_MOUSE	Q5rl10	mus musculu
35	8	2.6	139	2	Q2XGG0_PSEPU	Q2xgg0	pseudomonas
36	8	2.6	139	2	Q9KHT5_PSEPU	Q9kht5	pseudomonas
37	8	2.6	139	2	Q88ME0_PSEPK	Q88me0	pseudomonas
38	8	2.6	149	2	Q3BVP0_XANC5	Q3bvp0	xanthomonas
39	8	2.6	149	2	Q8PMN9_XANAC	Q8pmn9	xanthomonas
40	8	2.6	150	2	Q4HMH8_CAMLA	Q4hmh8	campylobact
41	8	2.6	159	2	Q43Z29_SOLUS	Q43z29	solibacter
42	8	2.6	161	2	Q3P6K2_9GAMM	Q3p6k2	shewanella
43	8	2.6	164	2	Q3X0V7_9ACTN	Q3x0v7	rubrobacter
44	8	2.6	181	1	AROL_SALTI	P63604	salmonella
45	8	2.6	181	1	AROL_SALTY	P63603	salmonella

#### ALIGNMENTS

#### RESULT 1

#### R4RL2\_HUMAN

ID R4RL2\_HUMAN STANDARD; PRT; 420 AA.  
AC Q86UN3; Q6X813;  
DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2003, sequence version 1.  
DT 07-MAR-2006, entry version 18.  
DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)  
DE (Nogo-66 receptor-related protein 2) (Ngr2) (Nogo receptor-like 3).  
GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=22581832; PubMed=12694398;  
RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,  
RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:08:00 ; Search time 137.627 Seconds  
(without alignments)  
930.199 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 1477  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1477	100.0	390	5	AAO21482	Aao21482 Mature hu
2	1477	100.0	390	7	ADF28529	Adf28529 NgRHy mat
3	1477	100.0	401	6	AAE33486	Aae33486 Human REM
4	1477	100.0	401	7	ADE07875	Ade07875 Novel pro
5	1477	100.0	401	7	ADF28528	Adf28528 NgRHy mut
6	1477	100.0	419	8	ADM72131	Adm72131 Human NTR
7	1477	100.0	420	5	AAO21477	Aao21477 Human NgR

8	1477	100.0	420	6	ABR55621	Abr55621	Amino aci
9	1477	100.0	420	7	ADF28510	Adf28510	NgRHy pre
10	1477	100.0	420	8	ADS10516	Ads10516	Human the
11	1461.5	99.0	512	7	ADC13559	Adc13559	Human NOV
12	1449	98.1	286	8	ADT77787	Adt77787	Rat Nogo
13	1449	98.1	420	6	ABR55628	Abr55628	Amino aci
14	1449	98.1	420	8	ADT77788	Adt77788	Rat Nogo
15	1449	98.1	452	8	ADT77808	Adt77808	Chimeric
16	1449	98.1	452	8	ADT77802	Adt77802	Chimeric
17	1449	98.1	474	8	ADT77796	Adt77796	Chimeric
18	1277.5	86.5	807	4	ABG15173	Abg15173	Novel hum
19	886	60.0	445	8	ADT77794	Adt77794	Rat Nogo
20	885	59.9	415	8	ADT77800	Adt77800	Chimeric
21	885	59.9	441	6	AAO27001	Aao27001	Human NgR
22	885	59.9	441	8	ADN12047	Adn12047	Novel hum
23	885	59.9	445	6	AAO27009	Aao27009	Rat NgRH2
24	885	59.9	445	8	ADN12049	Adn12049	Novel rat
25	885	59.9	445	8	ADT77790	Adt77790	Rat Nogo
26	885	59.9	473	8	ADT77795	Adt77795	Polypepti
27	879	59.5	421	5	AAO21483	Aao21483	Mature mo
28	879	59.5	461	5	AAO21478	Aao21478	Mouse NgR
29	791	53.6	392	5	AAO21487	Aao21487	Partial h
30	775.5	52.5	473	8	ADG75446	Adg75446	Macaque b
31	770.5	52.2	283	6	ABR59685	Abr59685	Human Nog
32	770.5	52.2	285	8	ADU21103	Adu21103	Human Nog
33	770.5	52.2	285	9	AEB19607	Aeb19607	Human sol
34	770.5	52.2	285	9	AEB86599	Aeb86599	Human NOG
35	770.5	52.2	310	8	ADM33975	Adm33975	Human Nog
36	770.5	52.2	310	9	ADY34441	Ady34441	Human Nog
37	770.5	52.2	310	9	AEB19598	Aeb19598	Human Nog
38	770.5	52.2	319	8	ADU21104	Adu21104	Human Nog
39	770.5	52.2	319	9	AEB19606	Aeb19606	Human sol
40	770.5	52.2	319	9	AEB86600	Aeb86600	Human NOG
41	770.5	52.2	344	8	ADM33974	Adm33974	Human Nog
42	770.5	52.2	344	8	ADU21101	Adu21101	Human Nog
43	770.5	52.2	344	9	ADY34440	Ady34440	Human Nog
44	770.5	52.2	344	9	AEB19597	Aeb19597	Human Nog
45	770.5	52.2	344	9	AEB86619	Aeb86619	Human NOG

# ALIGNMENTS

## RESULT 1

AAO21482

ID AAO21482 standard; protein; 390 AA.

XX

AC AAO21482;

XX

DT 15-AUG-2002 (first entry)

XX

DE Mature human NgR2 protein sequence.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;

KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;

KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;

KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:54:09 ; Search time 34.6441 Seconds  
 (without alignments)  
 707.439 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
 Perfect score: 1477  
 Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	770.5	52.2	473	2	US-09-949-016-8448	Sequence 8448, Ap
2	770.5	52.2	473	2	US-09-999-833A-400	Sequence 400, App
3	770.5	52.2	473	2	US-10-020-445A-400	Sequence 400, App
4	770.5	52.2	473	2	US-09-978-189-400	Sequence 400, App
5	770.5	52.2	473	2	US-10-017-085A-400	Sequence 400, App
6	770.5	52.2	473	3	US-10-145-129A-400	Sequence 400, App
7	770.5	52.2	473	3	US-10-013-929A-400	Sequence 400, App
8	770.5	52.2	473	3	US-10-013-917A-400	Sequence 400, App
9	767.5	52.0	380	2	US-09-461-325-161	Sequence 161, App
10	767.5	52.0	380	2	US-10-012-542-161	Sequence 161, App

11	767.5	52.0	380	2	US-10-115-123-161	Sequence 161, App
12	355	24.0	481	2	US-09-853-753-2	Sequence 2, Appli
13	355	24.0	485	2	US-09-949-016-8704	Sequence 8704, Ap
14	351	23.8	605	2	US-09-063-950-5	Sequence 5, Appli
15	349	23.6	605	1	US-08-190-802A-49	Sequence 49, Appl
16	349	23.6	605	2	US-08-477-346-49	Sequence 49, Appl
17	349	23.6	605	2	US-08-473-089-49	Sequence 49, Appl
18	349	23.6	605	2	US-08-487-072A-49	Sequence 49, Appl
19	349	23.6	605	2	US-09-538-092-1087	Sequence 1087, Ap
20	349	23.6	623	2	US-09-949-016-10995	Sequence 10995, A
21	337.5	22.9	545	3	US-10-114-270-38	Sequence 38, Appl
22	334.5	22.6	545	3	US-10-114-270-40	Sequence 40, Appl
23	330.5	22.4	498	2	US-10-188-495-51	Sequence 51, Appl
24	330.5	22.4	591	2	US-10-188-495-50	Sequence 50, Appl
25	330.5	22.4	622	2	US-10-188-495-48	Sequence 48, Appl
26	326	22.1	448	2	US-09-520-781-32	Sequence 32, Appl
27	326	22.1	448	2	US-09-957-187-32	Sequence 32, Appl
28	326	22.1	448	2	US-09-991-053-32	Sequence 32, Appl
29	326	22.1	590	2	US-09-520-781-12	Sequence 12, Appl
30	326	22.1	590	2	US-09-957-187-12	Sequence 12, Appl
31	326	22.1	590	2	US-09-991-053-12	Sequence 12, Appl
32	326	22.1	653	2	US-09-520-781-10	Sequence 10, Appl
33	326	22.1	653	2	US-09-957-187-10	Sequence 10, Appl
34	326	22.1	653	2	US-09-991-181-229	Sequence 229, App
35	326	22.1	653	2	US-09-990-444-229	Sequence 229, App
36	326	22.1	653	2	US-09-991-053-10	Sequence 10, Appl
37	326	22.1	653	2	US-09-997-333-229	Sequence 229, App
38	326	22.1	653	2	US-09-992-598-229	Sequence 229, App
39	326	22.1	653	2	US-09-989-735-229	Sequence 229, App
40	326	22.1	653	3	US-09-989-726-229	Sequence 229, App
41	326	22.1	653	3	US-09-997-514-229	Sequence 229, App
42	326	22.1	653	3	US-09-989-728-229	Sequence 229, App
43	326	22.1	653	3	US-09-997-349-229	Sequence 229, App
44	326	22.1	653	3	US-09-997-653-229	Sequence 229, App
45	326	22.1	653	3	US-09-989-293A-229	Sequence 229, App

#### ALIGNMENTS

##### RESULT 1

```

US-09-949-016-8448
; Sequence 8448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:24:49 ; Search time 117.695 Seconds  
(without alignments)  
1102.003 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 1477  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1477	100.0	390	3	US-09-972-546-8	Sequence 8, Appli
2	1477	100.0	390	5	US-10-735-256-8	Sequence 8, Appli
3	1477	100.0	390	5	US-10-496-905-439	Sequence 439, App
4	1477	100.0	401	5	US-10-477-714-17	Sequence 17, Appl
5	1477	100.0	401	5	US-10-496-905-438	Sequence 438, App
6	1477	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
7	1477	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
8	1477	100.0	420	5	US-10-496-905-420	Sequence 420, App
9	1477	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
10	1461.5	99.0	512	4	US-10-188-248-38	Sequence 38, Appl
11	1449	98.1	420	5	US-10-491-810A-25	Sequence 25, Appl

12	1277.5	86.5	807	5	US-10-450-763-45532	Sequence 45532, A
13	885	59.9	441	5	US-10-487-886-2	Sequence 2, Appli
14	885	59.9	445	5	US-10-487-886-25	Sequence 25, Appl
15	879	59.5	421	3	US-09-972-546-9	Sequence 9, Appli
16	879	59.5	421	5	US-10-735-256-9	Sequence 9, Appli
17	879	59.5	461	3	US-09-972-546-4	Sequence 4, Appli
18	879	59.5	461	5	US-10-735-256-4	Sequence 4, Appli
19	791	53.6	392	3	US-09-972-546-14	Sequence 14, Appl
20	791	53.6	392	5	US-10-735-256-14	Sequence 14, Appl
21	775.5	52.5	473	4	US-10-271-078-7	Sequence 7, Appli
22	770.5	52.2	283	3	US-09-972-599A-55	Sequence 55, Appl
23	770.5	52.2	310	6	US-11-055-163-7	Sequence 7, Appli
24	770.5	52.2	344	6	US-11-055-163-6	Sequence 6, Appli
25	770.5	52.2	473	3	US-09-758-140-2	Sequence 2, Appli
26	770.5	52.2	473	3	US-09-893-348-26	Sequence 26, Appl
27	770.5	52.2	473	3	US-09-972-599A-2	Sequence 2, Appli
28	770.5	52.2	473	3	US-09-978-295A-400	Sequence 400, App
29	770.5	52.2	473	3	US-09-978-697-400	Sequence 400, App
30	770.5	52.2	473	3	US-09-978-192A-400	Sequence 400, App
31	770.5	52.2	473	3	US-09-999-832A-400	Sequence 400, App
32	770.5	52.2	473	3	US-09-978-189-400	Sequence 400, App
33	770.5	52.2	473	3	US-09-978-608A-400	Sequence 400, App
34	770.5	52.2	473	3	US-09-978-585A-400	Sequence 400, App
35	770.5	52.2	473	3	US-09-978-191A-400	Sequence 400, App
36	770.5	52.2	473	3	US-09-978-403A-400	Sequence 400, App
37	770.5	52.2	473	3	US-09-978-564A-400	Sequence 400, App
38	770.5	52.2	473	3	US-09-999-833A-400	Sequence 400, App
39	770.5	52.2	473	3	US-09-981-915A-400	Sequence 400, App
40	770.5	52.2	473	3	US-09-978-824-400	Sequence 400, App
41	770.5	52.2	473	3	US-09-918-585A-400	Sequence 400, App
42	770.5	52.2	473	3	US-09-999-834A-400	Sequence 400, App
43	770.5	52.2	473	3	US-09-978-423A-400	Sequence 400, App
44	770.5	52.2	473	3	US-09-978-193A-400	Sequence 400, App
45	770.5	52.2	473	3	US-09-999-830A-400	Sequence 400, App

#### ALIGNMENTS

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RESULT 1
US-09-972-546-8
; Sequence 8, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116US
; CURRENT APPLICATION NUMBER: US/09/972,546
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 390

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 11:26:34 ; Search time 6.16949 Seconds  
(without alignments)  
1023.724 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 1477  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

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- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	333	22.5	811	6	US-10-505-928-32	Sequence 32, Appl
2	333	22.5	811	6	US-10-505-928-87	Sequence 87, Appl
3	325.5	22.0	673	7	US-11-101-316-16	Sequence 16, Appl
4	290	19.6	294	6	US-10-505-928-33	Sequence 33, Appl
5	283.5	19.2	1523	6	US-10-196-749-290	Sequence 290, App
6	272.5	18.4	513	7	US-11-101-316-124	Sequence 124, App
7	269	18.2	370	7	US-11-293-697-3248	Sequence 3248, Ap
8	259	17.5	598	7	US-11-296-092-69	Sequence 69, Appl
9	258.5	17.5	649	6	US-10-196-749-384	Sequence 384, App

10	258.5	17.5	649	7	US-11-101-316-132	Sequence 132, App
11	258	17.5	716	6	US-10-518-039-6	Sequence 6, Appli
12	258	17.5	812	6	US-10-518-039-5	Sequence 5, Appli
13	239	16.2	359	6	US-10-933-854-18	Sequence 18, Appl
14	238	16.1	719	7	US-11-293-697-3841	Sequence 3841, Ap
15	224.5	15.2	611	6	US-10-520-783-2	Sequence 2, Appli
16	222	15.0	745	7	US-11-293-697-3826	Sequence 3826, Ap
17	219.5	14.9	557	6	US-10-196-749-326	Sequence 326, App
18	211.5	14.3	379	7	US-11-296-092-2	Sequence 2, Appli
19	203	13.7	290	7	US-11-257-581-10	Sequence 10, Appl
20	203	13.7	302	7	US-11-257-581-7	Sequence 7, Appli
21	203	13.7	302	7	US-11-257-581-8	Sequence 8, Appli
22	203	13.7	531	7	US-11-257-581-4	Sequence 4, Appli
23	203	13.7	544	7	US-11-257-581-1	Sequence 1, Appli
24	203	13.7	544	7	US-11-257-581-2	Sequence 2, Appli
25	202.5	13.7	290	7	US-11-257-581-11	Sequence 11, Appl
26	202.5	13.7	290	7	US-11-257-581-12	Sequence 12, Appl
27	202.5	13.7	301	7	US-11-257-581-9	Sequence 9, Appli
28	202.5	13.7	531	7	US-11-257-581-5	Sequence 5, Appli
29	202.5	13.7	531	7	US-11-257-581-6	Sequence 6, Appli
30	202.5	13.7	544	7	US-11-257-581-3	Sequence 3, Appli
31	199.5	13.5	368	6	US-10-505-928-743	Sequence 743, App
32	189.5	12.8	703	7	US-11-291-140-4	Sequence 4, Appli
33	189.5	12.8	904	7	US-11-144-322-2	Sequence 2, Appli
34	189.5	12.8	904	7	US-11-291-140-2	Sequence 2, Appli
35	183	12.4	977	6	US-10-449-902-50526	Sequence 50526, A
36	180.5	12.2	692	6	US-10-196-749-560	Sequence 560, App
37	178.5	12.1	616	6	US-10-196-749-158	Sequence 158, App
38	178.5	12.1	1032	6	US-10-196-749-552	Sequence 552, App
39	171.5	11.6	1123	6	US-10-953-349-4749	Sequence 4749, Ap
40	169	11.4	1135	6	US-10-449-902-56546	Sequence 56546, A
41	168.5	11.4	501	6	US-10-449-902-48020	Sequence 48020, A
42	168	11.4	964	6	US-10-449-902-47345	Sequence 47345, A
43	167	11.3	546	6	US-10-196-749-412	Sequence 412, App
44	166.5	11.3	293	6	US-10-953-349-22365	Sequence 22365, A
45	166.5	11.3	598	6	US-10-953-349-7417	Sequence 7417, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-505-928-32

; Sequence 32, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 32

; LENGTH: 811

OM protein - protein search, using sw model

Run on: June 20, 2006, 10:51:54 ; Search time 12.8136 Seconds  
 (without alignments)  
 2102.514 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
 Perfect score: 1477  
 Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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 Listing first 45 summaries

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 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

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2	349	23.6	605	2	A41915	insulin-like growt
3	330.5	22.4	622	2	JC7973	synleurin - human
4	324.5	22.0	1469	2	B36665	slit protein 2 pre
5	324.5	22.0	1480	2	A36665	slit protein 1 pre
6	324	21.9	603	2	JC1282	insulin-like growt
7	321	21.7	603	2	JC6128	insulin-like growt
8	319	21.6	420	2	A53531	oncofetal trophobl
9	308	20.9	361	2	A53860	chondroadherin pre
10	297.5	20.1	1531	2	T42218	slit-1 protein hom
11	297	20.1	560	2	A60164	platelet membrane
12	280.5	19.0	312	1	NBHUA2	leucine-rich alpha
13	279.5	18.9	1523	2	T13953	MEGF5 protein - ra

14	278	18.8	707	2	JC7763	neuronal leucine-r
15	278	18.8	1091	2	A58532	glial cell membran
16	273.5	18.5	536	2	A34901	lysine carboxypept
17	255.5	17.3	360	2	S06280	decorin precursor
18	249.5	16.9	907	2	JE0176	orphan G protein-c
19	242.5	16.4	1535	2	S46224	peroxidasin - frui
20	240	16.2	789	2	T28714	hypothetical prote
21	240	16.2	1355	2	T28715	hypothetical prote
22	239	16.2	359	1	NBHUC8	decorin precursor
23	239	16.2	360	2	I47020	decorin - rabbit
24	236.5	16.0	354	2	S29145	decorin precursor
25	236.5	16.0	907	2	JG0193	G protein-coupled
26	235.5	15.9	1025	2	T42626	secreted leucine-r
27	234.5	15.9	357	2	S24317	decorin precursor
28	231.5	15.7	382	2	I39068	proline- arginine-
29	231.5	15.7	1112	2	T10504	disease resistance
30	231.5	15.7	1389	2	T13852	gene wheeler prote
31	228.5	15.5	1385	2	T13887	tlr protein - frui
32	227	15.4	662	2	S42799	garp precursor - h
33	227	15.4	682	2	A49121	cell-surface molec
34	227	15.4	682	2	A43318	connectin precurs
35	226.5	15.3	354	2	A55454	decorin precursor
36	222	15.0	562	2	T34319	hypothetical prote
37	220	14.9	594	2	T23841	hypothetical prote
38	220	14.9	610	2	T23836	hypothetical prote
39	217.5	14.7	738	2	T19938	hypothetical prote
40	211	14.3	1016	2	T30553	disease resistance
41	205.5	13.9	1066	2	T15864	hypothetical prote
42	204	13.8	1134	1	A29944	chaoptin precursor
43	203	13.7	626	1	NBHUIA	platelet glycoprot
44	199.5	13.5	368	1	BGHUN	biglycan precursor
45	199	13.5	375	2	S05390	fibromodulin precu

#### ALIGNMENTS

##### RESULT 1

JC5239

insulin-like growth factor acid-labile chain - baboon

C;Species: Papio sp. (baboon)

C;Date: 17-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-May-1997

C;Accession: JC5239

R;Delhanty, P.; Baxter, R.C.

Biochem. Biophys. Res. Commun. 227, 897-902, 1996

A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like growth factor binding protein complex.

A;Reference number: JC5239; MUID:97040714; PMID:8886027

A;Contents: liver

A;Accession: JC5239

A;Molecule type: mRNA

A;Residues: 1-605 <DEL>

A;Cross-references: UNIPARC:UPI000000D50E

C;Comment: This factor is structurally related to proinsulin and have insuline-like metabolic, differentiative, and cell proliferative activities.

Query Match

23.8%; Score 351; DB 2; Length 605;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 10:13:29 ; Search time 182.712 Seconds  
(without alignments)  
1417.556 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 1477  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	1449	98.1	420	1 R4RL2_MOUSE	Q7m6z0 mus musculu
3	1449	98.1	420	1 R4RL2_RAT	Q80wd1 rattus norv
4	935	63.3	411	2 Q4S6L6_TETNG	Q4s6l6 tetraodon n
5	923	62.5	457	2 Q6WZD1_BRARE	Q6wzd1 brachydanio
6	914	61.9	458	2 Q6WZD3_BRARE	Q6wzd3 brachydanio
7	906	61.3	478	2 Q6WZD2_BRARE	Q6wzd2 brachydanio
8	902.5	61.1	324	2 Q4S3K9_TETNG	Q4s3k9 tetraodon n
9	893	60.5	310	2 Q4RRQ4_TETNG	Q4rrq4 tetraodon n
10	885	59.9	441	1 R4RL1_HUMAN	Q86un2 homo sapien
11	885	59.9	445	1 R4RL1_RAT	Q80wd0 rattus norv
12	879	59.5	445	1 R4RL1_MOUSE	Q8k0s5 mus musculu
13	850	57.5	412	2 Q4RRU8_TETNG	Q4rru8 tetraodon n
14	797.5	54.0	479	2 Q6DH76_BRARE	Q6dh76 brachydanio
15	797.5	54.0	479	2 Q6X3Y5_BRARE	Q6x3y5 brachydanio

16	775.5	52.5	473	1	RTN4R_MACFA	Q9n0e3	macaca fasc
17	770.5	52.2	473	1	RTN4R_HUMAN	Q9bze6	homo sapien
18	754.5	51.1	473	1	RTN4R_RAT	Q99m75	rattus norv
19	740.5	50.1	473	1	RTN4R_MOUSE	Q99pi8	mus musculu
20	377.5	25.6	417	2	Q6E4J7_PETMA	Q6e4j7	petromyzon
21	365	24.7	290	2	Q2VGX3_PETMA	Q2vgx3	petromyzon
22	361.5	24.5	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
23	359.5	24.3	578	1	LRC15_RAT	Q8r5m3	rattus norv
24	355	24.0	481	1	NYX_HUMAN	Q9gzu5	homo sapien
25	355	24.0	481	2	Q2M1S4_HUMAN	Q2m1s4	homo sapien
26	355	24.0	637	2	Q6DCV7_XENLA	Q6dcv7	xenopus lae
27	352.5	23.9	264	2	Q2VGT2_PETMA	Q2vgt2	petromyzon
28	352.5	23.9	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
29	351.5	23.8	579	1	LRC15_MOUSE	Q80x72	mus musculu
30	351	23.8	513	2	Q50LG9_HUMAN	Q50lg9	homo sapien
31	351	23.8	605	1	ALS_PAPHA	O02833	papio hamad
32	350	23.7	605	2	Q8TAY0_HUMAN	Q8tay0	homo sapien
33	350	23.7	692	2	Q4G0S0_HUMAN	Q4g0s0	homo sapien
34	350	23.7	762	2	Q5JY13_HUMAN	Q5jy13	homo sapien
35	350	23.7	778	2	Q6NUI6_HUMAN	Q6nui6	homo sapien
36	349	23.6	605	1	ALS_HUMAN	P35858	homo sapien
37	348	23.6	521	2	Q8BHA1_MOUSE	Q8bha1	m 0 day neo
38	344.5	23.3	466	2	Q66IW3_XENLA	Q66iw3	xenopus lae
39	344	23.3	393	2	Q32R29_EPTBU	Q32r29	eptatretus
40	342	23.2	476	1	NYX_MOUSE	P83503	mus musculu
41	340	23.0	428	2	Q4S4W6_TETNG	Q4s4w6	tetraodon n
42	337.5	22.9	264	2	Q2VGV6_PETMA	Q2vgv6	petromyzon
43	337.5	22.9	545	1	CPN2_HUMAN	P22792	homo sapien
44	334	22.6	487	2	Q4SA13_TETNG	Q4sa13	tetraodon n
45	333	22.5	811	2	Q7L0X0_HUMAN	Q7l0x0	homo sapien

#### ALIGNMENTS

##### RESULT 1

##### R4RL2\_HUMAN

ID R4RL2\_HUMAN STANDARD; PRT; 420 AA.  
AC Q86UN3; Q6X813;  
DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2003, sequence version 1.  
DT 07-MAR-2006, entry version 18.  
DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)  
DE (Nogo-66 receptor-related protein 2) (NgR2) (Nogo receptor-like 3).  
GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=22581832; PubMed=12694398;  
RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,  
RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:43:57 ; Search time 229.695 Seconds  
(without alignments)  
557.351 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 280  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2588894

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
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9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	280	100.0	390	5	AAO21482	Aao21482 Mature hu
2	280	100.0	390	7	ADF28529	Adf28529 NgRHy mat
3	280	100.0	401	6	AAE33486	Aae33486 Human REM
4	280	100.0	401	7	ADE07875	Ade07875 Novel pro
5	280	100.0	401	7	ADF28528	Adf28528 NgRHy mut
6	280	100.0	419	8	ADM72131	Adm72131 Human NTR
7	280	100.0	420	5	AAO21477	Aao21477 Human NgR

8	280	100.0	420	6	ABR55621	Abr55621 Amino aci
9	280	100.0	420	7	ADF28510	Adf28510 NgRHy pre
10	280	100.0	420	8	ADS10516	Ads10516 Human the
11	141	50.4	286	8	ADT77787	Adt77787 Rat Nogo
12	141	50.4	420	6	ABR55628	Abr55628 Amino aci
13	141	50.4	420	8	ADT77788	Adt77788 Rat Nogo
14	141	50.4	452	8	ADT77808	Adt77808 Chimeric
15	141	50.4	452	8	ADT77802	Adt77802 Chimeric
16	141	50.4	474	8	ADT77796	Adt77796 Chimeric
17	140	50.0	512	7	ADC13559	Adc13559 Human NOV
18	133	47.5	241	4	ABG15171	Abg15171 Novel hum
19	126	45.0	807	4	ABG15173	Abg15173 Novel hum
20	50	17.9	51	7	ADF28526	Adf28526 Leucine-r
21	45	16.1	56	4	AAM23826	Aam23826 Human EST
22	45	16.1	56	7	ADE08958	Ade08958 Novel pro
23	45	16.1	56	8	ADS11791	Ads11791 Human the
24	33	11.8	492	4	ABG15172	Abg15172 Novel hum
25	25	8.9	25	7	ADF28520	Adf28520 Leucine-r
26	24	8.6	24	7	ADF28524	Adf28524 Leucine-r
27	24	8.6	24	7	ADF28525	Adf28525 Leucine-r
28	24	8.6	24	7	ADF28523	Adf28523 Leucine-r
29	24	8.6	24	7	ADF28522	Adf28522 Leucine-r
30	24	8.6	24	7	ADF28519	Adf28519 Leucine-r
31	24	8.6	24	7	ADF28521	Adf28521 Leucine-r
32	22	7.9	22	7	ADF28518	Adf28518 Leucine-r
33	15	5.4	15	7	ADF28513	Adf28513 PR00019A
34	15	5.4	15	7	ADF28515	Adf28515 PR00019A
35	15	5.4	15	7	ADF28516	Adf28516 PR00019B
36	15	5.4	15	7	ADF28514	Adf28514 PR00019B
37	15	5.4	15	7	ADF28517	Adf28517 PR00019B
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39	14	5.0	114	7	ADB47833	Adb47833 Novel hum
40	14	5.0	114	8	ADJ55388	Adj55388 Novel hum
41	14	5.0	114	9	AED67371	Aed67371 Human imm
42	11	3.9	11	8	ADT77816	Adt77816 Rat Nogo
43	11	3.9	49	6	ABR62021	Abr62021 Mouse Nog
44	11	3.9	49	6	ABR62022	Abr62022 Rat Nogo
45	11	3.9	49	6	ABR62020	Abr62020 Human Nog

#### ALIGNMENTS

##### RESULT 1

AAO21482

ID AAO21482 standard; protein; 390 AA.

XX

AC AAO21482;

XX

DT 15-AUG-2002 (first entry)

XX

DE Mature human NgR2 protein sequence.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;

KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;

KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;

KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:59:16 ; Search time 33.6949 Seconds  
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Title: US-10-735-256-2\_COPY\_31\_310  
Perfect score: 280  
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	14	5.0	115	2	US-09-774-639-154	Sequence 154, App
2	11	3.9	380	2	US-09-461-325-161	Sequence 161, App
3	11	3.9	380	2	US-10-012-542-161	Sequence 161, App
4	11	3.9	380	2	US-10-115-123-161	Sequence 161, App
5	11	3.9	473	2	US-09-949-016-8448	Sequence 8448, Ap
6	11	3.9	473	2	US-09-999-833A-400	Sequence 400, App
7	11	3.9	473	2	US-10-020-445A-400	Sequence 400, App
8	11	3.9	473	2	US-09-978-189-400	Sequence 400, App
9	11	3.9	473	2	US-10-017-085A-400	Sequence 400, App
10	11	3.9	473	3	US-10-145-129A-400	Sequence 400, App

11	11	3.9	473	3	US-10-013-929A-400	Sequence 400, App
12	11	3.9	473	3	US-10-013-917A-400	Sequence 400, App
13	8	2.9	226	2	US-09-489-039A-10549	Sequence 10549, A
14	8	2.9	320	2	US-09-248-796A-16573	Sequence 16573, A
15	8	2.9	446	2	US-09-252-991A-23809	Sequence 23809, A
16	8	2.9	455	2	US-09-793-998-8	Sequence 8, Appli
17	8	2.9	799	3	US-09-396-985B-4	Sequence 4, Appli
18	8	2.9	839	3	US-09-396-985B-2	Sequence 2, Appli
19	8	2.9	839	3	US-09-396-985B-98	Sequence 98, Appl
20	8	2.9	844	2	US-09-949-016-9438	Sequence 9438, Ap
21	8	2.9	990	2	US-10-101-464A-814	Sequence 814, App
22	7	2.5	70	2	US-09-107-532A-4266	Sequence 4266, Ap
23	7	2.5	150	2	US-09-270-767-34661	Sequence 34661, A
24	7	2.5	150	2	US-09-270-767-49878	Sequence 49878, A
25	7	2.5	185	2	US-10-101-464A-519	Sequence 519, App
26	7	2.5	213	2	US-09-328-352-6050	Sequence 6050, Ap
27	7	2.5	222	2	US-09-248-796A-15754	Sequence 15754, A
28	7	2.5	260	2	US-09-902-540-10767	Sequence 10767, A
29	7	2.5	268	2	US-10-104-047-3172	Sequence 3172, Ap
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32	7	2.5	271	2	US-09-902-540-11216	Sequence 11216, A
33	7	2.5	283	2	US-09-252-991A-27181	Sequence 27181, A
34	7	2.5	291	2	US-09-134-001C-3893	Sequence 3893, Ap
35	7	2.5	310	2	US-10-094-749-3057	Sequence 3057, Ap
36	7	2.5	320	2	US-09-325-932A-190	Sequence 190, App
37	7	2.5	322	2	US-10-101-464A-648	Sequence 648, App
38	7	2.5	326	2	US-09-252-991A-18751	Sequence 18751, A
39	7	2.5	354	2	US-09-067-089-2	Sequence 2, Appli
40	7	2.5	354	2	US-09-574-377-32	Sequence 32, Appl
41	7	2.5	354	2	US-09-574-377-33	Sequence 33, Appl
42	7	2.5	354	2	US-10-184-194-32	Sequence 32, Appl
43	7	2.5	354	2	US-10-184-194-33	Sequence 33, Appl
44	7	2.5	354	3	US-10-932-269-2	Sequence 2, Appli
45	7	2.5	356	1	US-08-270-583-2	Sequence 2, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-774-639-154

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; Sequence 154, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 115
; TYPE: PRT
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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:15:51 ; Search time 116.746 Seconds  
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 1110.962 Million cell updates/sec

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Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096261

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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		Match	Length			
1	280	100.0	390	3	US-09-972-546-8	Sequence 8, Appli
2	280	100.0	390	5	US-10-735-256-8	Sequence 8, Appli
3	280	100.0	390	5	US-10-496-905-439	Sequence 439, App
4	280	100.0	401	5	US-10-477-714-17	Sequence 17, Appl
5	280	100.0	401	5	US-10-496-905-438	Sequence 438, App
6	280	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
7	280	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
8	280	100.0	420	5	US-10-496-905-420	Sequence 420, App
9	280	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
10	141	50.4	420	5	US-10-491-810A-25	Sequence 25, Appl
11	140	50.0	512	4	US-10-188-248-38	Sequence 38, Appl

12	133	47.5	241	5	US-10-450-763-45530	Sequence 45530, A
13	126	45.0	807	5	US-10-450-763-45532	Sequence 45532, A
14	50	17.9	51	5	US-10-496-905-436	Sequence 436, App
15	33	11.8	492	5	US-10-450-763-45531	Sequence 45531, A
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17	24	8.6	24	5	US-10-496-905-429	Sequence 429, App
18	24	8.6	24	5	US-10-496-905-431	Sequence 431, App
19	24	8.6	24	5	US-10-496-905-432	Sequence 432, App
20	24	8.6	24	5	US-10-496-905-433	Sequence 433, App
21	24	8.6	24	5	US-10-496-905-434	Sequence 434, App
22	24	8.6	24	5	US-10-496-905-435	Sequence 435, App
23	22	7.9	22	5	US-10-496-905-428	Sequence 428, App
24	15	5.4	15	5	US-10-496-905-423	Sequence 423, App
25	15	5.4	15	5	US-10-496-905-424	Sequence 424, App
26	15	5.4	15	5	US-10-496-905-425	Sequence 425, App
27	15	5.4	15	5	US-10-496-905-426	Sequence 426, App
28	15	5.4	15	5	US-10-496-905-427	Sequence 427, App
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39	11	3.9	283	3	US-09-972-599A-55	Sequence 55, Appl
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42	11	3.9	344	6	US-11-055-163-6	Sequence 6, Appli
43	11	3.9	344	6	US-11-055-163-8	Sequence 8, Appli
44	11	3.9	380	4	US-10-012-542-161	Sequence 161, App
45	11	3.9	380	4	US-10-115-123-161	Sequence 161, App

#### ALIGNMENTS

RESULT 1  
 US-09-972-546-8  
 ; Sequence 8, Application US/09972546  
 ; Publication No. US20030124704A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRITTMATTER, STEPHEN M.  
 ; APPLICANT: CATE, RICHARD L.  
 ; APPLICANT: SAH, DINAH W.Y.  
 ; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS  
 ; FILE REFERENCE: A116US  
 ; CURRENT APPLICATION NUMBER: US/09/972,546  
 ; CURRENT FILING DATE: 2001-10-06  
 ; PRIOR APPLICATION NUMBER: 60/238,361  
 ; PRIOR FILING DATE: 2000-10-06  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 390

OM protein - protein search, using sw model

Run on: June 20, 2006, 12:16:16 ; Search time 12.339 Seconds  
 (without alignments)  
 511.862 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
 Perfect score: 280  
 Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 96747 seqs, 22556637 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96734

Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
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5	7	2.5	319	6	US-10-449-902-45409	Sequence 45409, A
6	7	2.5	330	6	US-10-953-349-5740	Sequence 5740, Ap
7	7	2.5	332	6	US-10-953-349-5739	Sequence 5739, Ap
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9	7	2.5	503	6	US-10-953-349-26067	Sequence 26067, A

10	7	2.5	587	7	US-11-293-697-4811	Sequence 4811, Ap
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12	7	2.5	621	7	US-11-106-014-56	Sequence 56, Appl
13	7	2.5	719	7	US-11-293-697-3841	Sequence 3841, Ap
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15	6	2.1	11	7	US-11-122-986-354	Sequence 354, App
16	6	2.1	30	7	US-11-122-986-829	Sequence 829, App
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44	6	2.1	158	6	US-10-953-349-36533	Sequence 36533, A
45	6	2.1	158	6	US-10-449-902-30737	Sequence 30737, A

#### ALIGNMENTS

#### RESULT 1

US-10-449-902-34272

; Sequence 34272, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:52:46 ; Search time 24.2034 Seconds  
 (without alignments)  
 1113.096 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
 Perfect score: 280  
 Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	8	2.9	181	2	AC0550	shikimate kinase I
2	8	2.9	244	2	JC8019	CD58 protein - pig
3	8	2.9	262	1	B64154	probable radical-f
4	8	2.9	481	2	T33733	hypothetical prote
5	8	2.9	925	2	H96638	protein T1F9.20 [i
6	8	2.9	967	2	G96637	hypothetical prote
7	8	2.9	1148	2	D85360	hypothetical prote
8	7	2.5	60	2	AD2255	hypothetical prote
9	7	2.5	62	2	T28346	ORF MSV185 hypothe
10	7	2.5	83	2	D70639	hypothetical prote
11	7	2.5	132	1	B64104	virulence-associat
12	7	2.5	147	1	HBLUA	hemoglobin beta ch
13	7	2.5	154	2	T07767	disease resistance

14	7	2.5	154	2	T07769	disease resistance
15	7	2.5	157	2	G84292	hypothetical prote
16	7	2.5	164	2	T51261	hypothetical prote
17	7	2.5	212	2	B75156	resolvase related
18	7	2.5	216	2	T37221	hypothetical prote
19	7	2.5	219	2	F83160	two-component resp
20	7	2.5	223	2	E83596	DNA mismatch repai
21	7	2.5	225	2	T11279	H <sup>+</sup> -transporting tw
22	7	2.5	237	2	T26765	hypothetical prote
23	7	2.5	250	2	S75302	hypothetical prote
24	7	2.5	252	2	T01787	thyrotropin recept
25	7	2.5	253	1	JC1319	thyrotropin recept
26	7	2.5	253	2	T00290	psiA protein - Esc
27	7	2.5	260	2	T18554	integral membrane
28	7	2.5	264	2	G83245	probable ATP-bindi
29	7	2.5	283	2	E83053	dihydropteroate sy
30	7	2.5	285	2	A40657	hypothetical prote
31	7	2.5	310	2	T44912	cysteine synthase
32	7	2.5	320	2	T47882	hypothetical prote
33	7	2.5	326	2	D84088	cytosine-specific
34	7	2.5	326	2	C82200	cytochrome c oxida
35	7	2.5	329	2	T17033	leucine rich repea
36	7	2.5	332	2	T47703	Ca-dependent solut
37	7	2.5	343	2	D83839	glucose-resistance
38	7	2.5	351	2	F64880	ycjS protein - Esc
39	7	2.5	356	1	A54038	phenylalanine dehy
40	7	2.5	360	2	C84243	asparagine synthet
41	7	2.5	365	2	F87552	dprA protein [impo
42	7	2.5	383	2	AH2516	hypothetical prote
43	7	2.5	390	2	T35509	hypothetical prote
44	7	2.5	403	2	S58345	E2F-1 transcriptio
45	7	2.5	420	2	T50585	probable membrane

#### ALIGNMENTS

##### RESULT 1

AC0550

shikimate kinase II [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C;Accession: AC0550

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

OM protein - protein search, using sw model

Run on: June 20, 2006, 11:44:20 ; Search time 182.237 Seconds  
 (without alignments)  
 1421.248 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_31\_310  
 Perfect score: 280  
 Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_7.2:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	280	100.0	420	1 R4RL2_HUMAN	Q86un3 homo sapien
2	141	50.4	420	1 R4RL2_RAT	Q80wd1 rattus norv
3	125	44.6	420	1 R4RL2_MOUSE	Q7m6z0 mus musculu
4	12	4.3	310	2 Q4RRQ4_TETNG	Q4rrq4 tetraodon n
5	12	4.3	324	2 Q4S3K9_TETNG	Q4s3k9 tetraodon n
6	12	4.3	411	2 Q4S6L6_TETNG	Q4s6l6 tetraodon n
7	12	4.3	412	2 Q4RRU8_TETNG	Q4rru8 tetraodon n
8	12	4.3	457	2 Q6WZD1_BRARE	Q6wzd1 brachydanio
9	12	4.3	478	2 Q6WZD2_BRARE	Q6wzd2 brachydanio
10	11	3.9	473	1 RTN4R_HUMAN	Q9bZR6 homo sapien
11	11	3.9	473	1 RTN4R_MACFA	Q9n0e3 macaca fasc
12	11	3.9	473	1 RTN4R_MOUSE	Q99pi8 mus musculu
13	11	3.9	473	1 RTN4R_RAT	Q99m75 rattus norv
14	10	3.6	441	1 R4RL1_HUMAN	Q86un2 homo sapien
15	10	3.6	445	1 R4RL1_MOUSE	Q8k0s5 mus musculu

16	10	3.6	445	1	R4RL1_RAT	Q80wd0	rattus norv
17	9	3.2	321	2	Q3MSG3_KLEOX	Q3msg3	klebsiella
18	9	3.2	321	2	Q3MSI6_KLEPN	Q3msi6	klebsiella
19	9	3.2	400	2	Q45WB1_TOXGO	Q45wb1	toxoplasma
20	9	3.2	458	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
21	9	3.2	479	2	Q6DH76_BRARE	Q6dh76	brachydanio
22	9	3.2	479	2	Q6X3Y5_BRARE	Q6x3y5	brachydanio
23	9	3.2	686	2	Q5FLT7_LACAC	Q5flt7	lactobacill
24	9	3.2	1207	2	Q2JZJ1_RHIET	Q2jzj1	rhizobium e
25	8	2.9	93	2	Q3ITV5_NATPD	Q3itv5	natronomona
26	8	2.9	150	2	Q4HMH8_CAMLA	Q4hmh8	campylobact
27	8	2.9	161	2	Q3P6K2_9GAMM	Q3p6k2	shewanella
28	8	2.9	181	1	AROL_SALTI	P63604	salmonella
29	8	2.9	181	1	AROL_SALTY	P63603	salmonella
30	8	2.9	181	2	Q57SH6_SALCH	Q57sh6	salmonella
31	8	2.9	181	2	Q5PFV5_SALPA	Q5pfv5	salmonella
32	8	2.9	197	2	Q4IYH4_AZOVI	Q4iyh4	azotobacter
33	8	2.9	210	1	KGUA_IDILO	Q5qyh9	idiomarina
34	8	2.9	216	2	Q5SKH3_THET8	Q5skh3	thermus the
35	8	2.9	219	2	Q7FAK9_ORYSA	Q7fak9	oryza sativ
36	8	2.9	228	2	Q8SAS9_SOYBN	Q8sas9	glycine max
37	8	2.9	241	2	Q5UCB1_TRYCR	Q5ucb1	trypanosoma
38	8	2.9	244	2	Q7YS40_PIG	Q7ys40	sus scrofa
39	8	2.9	244	2	Q8SQB6_PIG	Q8sqb6	sus scrofa
40	8	2.9	246	2	Q72KM2_THET2	Q72km2	thermus the
41	8	2.9	262	1	Y520_HAEIN	P44743	haemophilus
42	8	2.9	262	2	Q4QN28_HAEI8	Q4qn28	haemophilus
43	8	2.9	280	2	Q2RVY3_RHORU	Q2rvy3	rhodospiril
44	8	2.9	280	2	Q4BSV7_BURVI	Q4bsv7	burkholderi
45	8	2.9	280	2	Q81D98_BACCR	Q81d98	bacillus ce

#### ALIGNMENTS

##### RESULT 1

##### R4RL2\_HUMAN

ID R4RL2\_HUMAN STANDARD; PRT; 420 AA.  
AC Q86UN3; Q6X813;  
DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2003, sequence version 1.  
DT 07-MAR-2006, entry version 18.  
DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)  
DE (Nogo-66 receptor-related protein 2) (NgR2) (Nogo receptor-like 3).  
GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Brain;  
RX MEDLINE=22581832; PubMed=12694398;  
RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,  
RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;

OM protein - protein search, using sw model

Run on: June 20, 2006, 10:08:00 ; Search time 152.373 Seconds  
 (without alignments)  
 930.199 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
 Perfect score: 1621  
 Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*  
 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1621	100.0	401	7	ADF28528 NgRHy mut
2	1621	100.0	420	5	AAO21477 Human NgR
3	1621	100.0	420	6	ABR55621 Amino aci
4	1621	100.0	420	7	ADF28510 NgRHy pre
5	1621	100.0	420	8	ADS10516 Human the
6	1576	97.2	419	8	ADM72131 Human NTR
7	1568	96.7	420	6	ABR55628 Amino aci

8	1568	96.7	420	8	ADT77788	Adt77788	Rat Nogo
9	1568	96.7	452	8	ADT77808	Adt77808	Chimeric
10	1568	96.7	452	8	ADT77802	Adt77802	Chimeric
11	1568	96.7	474	8	ADT77796	Adt77796	Chimeric
12	1528	94.3	401	6	AAE33486	Aae33486	Human REM
13	1528	94.3	401	7	ADE07875	Ade07875	Novel pro
14	1512.5	93.3	512	7	ADC13559	Adc13559	Human NOV
15	1477	91.1	390	5	AAO21482	Aao21482	Mature hu
16	1477	91.1	390	7	ADF28529	Adf28529	NgRHy mat
17	1460	90.1	286	8	ADT77787	Adt77787	Rat Nogo
18	1372.5	84.7	807	4	ABG15173	Abg15173	Novel hum
19	906.5	55.9	445	8	ADT77794	Adt77794	Rat Nogo
20	905.5	55.9	415	8	ADT77800	Adt77800	Chimeric
21	905.5	55.9	445	6	AAO27009	Aao27009	Rat NgRH2
22	905.5	55.9	445	8	ADN12049	Adn12049	Novel rat
23	905.5	55.9	445	8	ADT77790	Adt77790	Rat Nogo
24	903	55.7	461	5	AAO21478	Aao21478	Mouse NgR
25	901.5	55.6	441	6	AAO27001	Aao27001	Human NgR
26	901.5	55.6	441	8	ADN12047	Adn12047	Novel hum
27	901.5	55.6	473	8	ADT77795	Adt77795	Polypepti
28	879	54.2	421	5	AAO21483	Aao21483	Mature mo
29	791	48.8	392	5	AAO21487	Aao21487	Partial h
30	787	48.6	473	8	ADG75446	Adg75446	Macaque b
31	783	48.3	310	8	ADM33975	Adm33975	Human Nog
32	783	48.3	310	9	ADY34441	Ady34441	Human Nog
33	783	48.3	310	9	AEB19598	Aeb19598	Human Nog
34	783	48.3	344	8	ADM33974	Adm33974	Human Nog
35	783	48.3	344	8	ADU21101	Adu21101	Human Nog
36	783	48.3	344	9	ADY34440	Ady34440	Human Nog
37	783	48.3	344	9	AEB19597	Aeb19597	Human Nog
38	783	48.3	344	9	AEB86619	Aeb86619	Human NOG
39	783	48.3	472	3	AAB33426	Aab33426	Human PRO
40	783	48.3	473	2	AAY41745	Aay41745	Human PRO
41	783	48.3	473	3	AAB44301	Aab44301	Human PRO
42	783	48.3	473	3	AAB24410	Aab24410	Human PRO
43	783	48.3	473	3	AAY95345	Aay95345	Human PRO
44	783	48.3	473	4	AAU12362	Aau12362	Human PRO
45	783	48.3	473	4	AAU04589	Aau04589	Human Nog

# ALIGNMENTS

## RESULT 1

ADF28528

ID ADF28528 standard; protein; 401 AA.

XX

AC ADF28528;

XX

DT 12-FEB-2004 (first entry)

XX

DE NgRHy mutant protein lacking transmembrane domain - SED ID 438.

XX

KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;

KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;

KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;

KW paralysis; seizure; memory disorder; adiponectin; Clq domain;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:54:09 ; Search time 38.3559 Seconds  
(without alignments)  
707.439 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 1621  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	783	48.3	473	2	US-09-949-016-8448	Sequence 8448, Ap
2	783	48.3	473	2	US-09-999-833A-400	Sequence 400, App
3	783	48.3	473	2	US-10-020-445A-400	Sequence 400, App
4	783	48.3	473	2	US-09-978-189-400	Sequence 400, App
5	783	48.3	473	2	US-10-017-085A-400	Sequence 400, App
6	783	48.3	473	3	US-10-145-129A-400	Sequence 400, App
7	783	48.3	473	3	US-10-013-929A-400	Sequence 400, App
8	783	48.3	473	3	US-10-013-917A-400	Sequence 400, App
9	780	48.1	380	2	US-09-461-325-161	Sequence 161, App
10	780	48.1	380	2	US-10-012-542-161	Sequence 161, App

11	780	48.1	380	2	US-10-115-123-161	Sequence 161, App
12	369	22.8	481	2	US-09-853-753-2	Sequence 2, Appli
13	369	22.8	485	2	US-09-949-016-8704	Sequence 8704, Ap
14	357	22.0	545	3	US-10-114-270-38	Sequence 38, Appl
15	354	21.8	545	3	US-10-114-270-40	Sequence 40, Appl
16	353	21.8	605	2	US-09-063-950-5	Sequence 5, Appli
17	349.5	21.6	622	2	US-10-188-495-48	Sequence 48, Appl
18	349	21.5	605	1	US-08-190-802A-49	Sequence 49, Appl
19	349	21.5	605	2	US-08-477-346-49	Sequence 49, Appl
20	349	21.5	605	2	US-08-473-089-49	Sequence 49, Appl
21	349	21.5	605	2	US-08-487-072A-49	Sequence 49, Appl
22	349	21.5	605	2	US-09-538-092-1087	Sequence 1087, Ap
23	349	21.5	623	2	US-09-949-016-10995	Sequence 10995, A
24	345.5	21.3	673	2	US-09-063-950-2	Sequence 2, Appli
25	345.5	21.3	673	2	US-09-991-181-52	Sequence 52, Appl
26	345.5	21.3	673	2	US-09-990-444-52	Sequence 52, Appl
27	345.5	21.3	673	2	US-09-997-333-52	Sequence 52, Appl
28	345.5	21.3	673	2	US-09-992-598-52	Sequence 52, Appl
29	345.5	21.3	673	2	US-09-989-735-52	Sequence 52, Appl
30	345.5	21.3	673	3	US-09-989-726-52	Sequence 52, Appl
31	345.5	21.3	673	3	US-09-997-514-52	Sequence 52, Appl
32	345.5	21.3	673	3	US-09-989-728-52	Sequence 52, Appl
33	345.5	21.3	673	3	US-09-997-349-52	Sequence 52, Appl
34	345.5	21.3	673	3	US-09-997-653-52	Sequence 52, Appl
35	345.5	21.3	673	3	US-09-989-293A-52	Sequence 52, Appl
36	333.5	20.6	640	2	US-09-907-794A-292	Sequence 292, App
37	333.5	20.6	640	2	US-09-905-125A-292	Sequence 292, App
38	333.5	20.6	640	2	US-09-902-775A-292	Sequence 292, App
39	333.5	20.6	640	2	US-09-906-700-292	Sequence 292, App
40	333.5	20.6	640	2	US-09-903-603A-292	Sequence 292, App
41	333.5	20.6	640	2	US-09-904-920A-292	Sequence 292, App
42	333.5	20.6	640	2	US-09-909-064-292	Sequence 292, App
43	333.5	20.6	640	2	US-09-905-381A-292	Sequence 292, App
44	333.5	20.6	640	2	US-09-906-618-292	Sequence 292, App
45	333.5	20.6	640	2	US-09-906-646-292	Sequence 292, App

# ALIGNMENTS

## RESULT 1

US-09-949-016-8448

; Sequence 8448, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498



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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:24:49 ; Search time 130.305 Seconds  
(without alignments)  
1102.003 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 1621  
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1621	100.0	401	5	US-10-496-905-438	Sequence 438, App
2	1621	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
3	1621	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
4	1621	100.0	420	5	US-10-496-905-420	Sequence 420, App
5	1621	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
6	1568	96.7	420	5	US-10-491-810A-25	Sequence 25, Appl
7	1528	94.3	401	5	US-10-477-714-17	Sequence 17, Appl
8	1512.5	93.3	512	4	US-10-188-248-38	Sequence 38, Appl
9	1477	91.1	390	3	US-09-972-546-8	Sequence 8, Appli
10	1477	91.1	390	5	US-10-735-256-8	Sequence 8, Appli
11	1477	91.1	390	5	US-10-496-905-439	Sequence 439, App

12	1372.5	84.7	807	5	US-10-450-763-45532	Sequence 45532, A
13	905.5	55.9	445	5	US-10-487-886-25	Sequence 25, Appl
14	903	55.7	461	3	US-09-972-546-4	Sequence 4, Appli
15	903	55.7	461	5	US-10-735-256-4	Sequence 4, Appli
16	901.5	55.6	441	5	US-10-487-886-2	Sequence 2, Appli
17	879	54.2	421	3	US-09-972-546-9	Sequence 9, Appli
18	879	54.2	421	5	US-10-735-256-9	Sequence 9, Appli
19	791	48.8	392	3	US-09-972-546-14	Sequence 14, Appl
20	791	48.8	392	5	US-10-735-256-14	Sequence 14, Appl
21	787	48.6	473	4	US-10-271-078-7	Sequence 7, Appli
22	783	48.3	310	6	US-11-055-163-7	Sequence 7, Appli
23	783	48.3	344	6	US-11-055-163-6	Sequence 6, Appli
24	783	48.3	473	3	US-09-758-140-2	Sequence 2, Appli
25	783	48.3	473	3	US-09-893-348-26	Sequence 26, Appl
26	783	48.3	473	3	US-09-972-599A-2	Sequence 2, Appli
27	783	48.3	473	3	US-09-978-295A-400	Sequence 400, App
28	783	48.3	473	3	US-09-978-697-400	Sequence 400, App
29	783	48.3	473	3	US-09-978-192A-400	Sequence 400, App
30	783	48.3	473	3	US-09-999-832A-400	Sequence 400, App
31	783	48.3	473	3	US-09-978-189-400	Sequence 400, App
32	783	48.3	473	3	US-09-978-608A-400	Sequence 400, App
33	783	48.3	473	3	US-09-978-585A-400	Sequence 400, App
34	783	48.3	473	3	US-09-978-191A-400	Sequence 400, App
35	783	48.3	473	3	US-09-978-403A-400	Sequence 400, App
36	783	48.3	473	3	US-09-978-564A-400	Sequence 400, App
37	783	48.3	473	3	US-09-999-833A-400	Sequence 400, App
38	783	48.3	473	3	US-09-981-915A-400	Sequence 400, App
39	783	48.3	473	3	US-09-978-824-400	Sequence 400, App
40	783	48.3	473	3	US-09-918-585A-400	Sequence 400, App
41	783	48.3	473	3	US-09-999-834A-400	Sequence 400, App
42	783	48.3	473	3	US-09-978-423A-400	Sequence 400, App
43	783	48.3	473	3	US-09-978-193A-400	Sequence 400, App
44	783	48.3	473	3	US-09-999-830A-400	Sequence 400, App
45	783	48.3	473	3	US-09-978-757A-400	Sequence 400, App

#### ALIGNMENTS

##### RESULT 1

US-10-496-905-438

; Sequence 438, Application US/10496905

; Publication No. US20050192215A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Malabika

; APPLICANT: Tang, Y. Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Zhao, Qing

; APPLICANT: Xu, Chongjun

; APPLICANT: Mulero, Julio J

; APPLICANT: Boyle, Bryan J.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

; FILE REFERENCE: HYS-B1CIP/US

; CURRENT APPLICATION NUMBER: US/10/496,905

; CURRENT FILING DATE: 2004-05-26

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:26:34 ; Search time 6.83051 Seconds  
(without alignments)  
1023.724 Million cell updates/sec

Title: US-10-735-256-2\_COPY\_1\_310  
Perfect score: 1621  
Sequence: 1 MLPGLRRLQLQAPASACILLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	359	22.1	811	6	US-10-505-928-32	Sequence 32, Appl
2	359	22.1	811	6	US-10-505-928-87	Sequence 87, Appl
3	345.5	21.3	673	7	US-11-101-316-16	Sequence 16, Appl
4	311.5	19.2	294	6	US-10-505-928-33	Sequence 33, Appl
5	295	18.2	1523	6	US-10-196-749-290	Sequence 290, App
6	288	17.8	513	7	US-11-101-316-124	Sequence 124, App
7	280	17.3	370	7	US-11-293-697-3248	Sequence 3248, Ap
8	279	17.2	598	7	US-11-296-092-69	Sequence 69, Appl
9	275.5	17.0	649	6	US-10-196-749-384	Sequence 384, App

10	275.5	17.0	649	7	US-11-101-316-132	Sequence 132, App
11	267.5	16.5	812	6	US-10-518-039-5	Sequence 5, Appli
12	266	16.4	716	6	US-10-518-039-6	Sequence 6, Appli
13	250	15.4	719	7	US-11-293-697-3841	Sequence 3841, Ap
14	248	15.3	359	6	US-10-933-854-18	Sequence 18, Appl
15	234.5	14.5	557	6	US-10-196-749-326	Sequence 326, App
16	232	14.3	745	7	US-11-293-697-3826	Sequence 3826, Ap
17	226.5	14.0	611	6	US-10-520-783-2	Sequence 2, Appli
18	218.5	13.5	531	7	US-11-257-581-4	Sequence 4, Appli
19	218.5	13.5	544	7	US-11-257-581-1	Sequence 1, Appli
20	218.5	13.5	544	7	US-11-257-581-2	Sequence 2, Appli
21	218	13.4	531	7	US-11-257-581-5	Sequence 5, Appli
22	218	13.4	531	7	US-11-257-581-6	Sequence 6, Appli
23	218	13.4	544	7	US-11-257-581-3	Sequence 3, Appli
24	217.5	13.4	379	7	US-11-296-092-2	Sequence 2, Appli
25	203	12.5	290	7	US-11-257-581-10	Sequence 10, Appl
26	203	12.5	302	7	US-11-257-581-7	Sequence 7, Appli
27	203	12.5	302	7	US-11-257-581-8	Sequence 8, Appli
28	202.5	12.5	290	7	US-11-257-581-11	Sequence 11, Appl
29	202.5	12.5	290	7	US-11-257-581-12	Sequence 12, Appl
30	202.5	12.5	301	7	US-11-257-581-9	Sequence 9, Appli
31	202.5	12.5	368	6	US-10-505-928-743	Sequence 743, App
32	189.5	11.7	703	7	US-11-291-140-4	Sequence 4, Appli
33	189.5	11.7	904	7	US-11-144-322-2	Sequence 2, Appli
34	189.5	11.7	904	7	US-11-291-140-2	Sequence 2, Appli
35	187	11.5	977	6	US-10-449-902-50526	Sequence 50526, A
36	180.5	11.1	692	6	US-10-196-749-560	Sequence 560, App
37	178.5	11.0	616	6	US-10-196-749-158	Sequence 158, App
38	178.5	11.0	1032	6	US-10-196-749-552	Sequence 552, App
39	171.5	10.6	1123	6	US-10-953-349-4749	Sequence 4749, Ap
40	171	10.5	298	7	US-11-297-134-25	Sequence 25, Appl
41	170.5	10.5	1074	6	US-10-449-902-52953	Sequence 52953, A
42	169	10.4	1135	6	US-10-449-902-56546	Sequence 56546, A
43	168.5	10.4	501	6	US-10-449-902-48020	Sequence 48020, A
44	168	10.4	964	6	US-10-449-902-47345	Sequence 47345, A
45	167	10.3	546	6	US-10-196-749-412	Sequence 412, App

#### ALIGNMENTS

##### RESULT 1

US-10-505-928-32

; Sequence 32, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 32

; LENGTH: 811